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TITLE

HUMAN CHEMOKINE BETA-9

This is to certify that annexed hereto is a true copy from the records of the United States Patent and Trademark Office of the application which is identified above.

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Human Chemokine Beta-9

This invention relates to newly identified polynucleotides, polypeptides encoded by such polynucleotides, the use of such polynucleotides and polypeptides, as well as the production of such polynucleotides and polypeptides. More particularly, the polypeptides of the present invention are human chemokine beta-9 sometimes hereinafter referred to as "Ckβ-9". The invention also relates to inhibiting the action of such polypeptides.

Chemokines are an emerging super-family of small secreted cytokines that are structurally and functionally related. All chemokines exhibit 25 to 75% homology at the amino acid level and contain spatially conserved cysteine residues as do the polypeptides of the present invention. Members of the "C-X-C branch" (according to the position of the first two cysteines in the conserved motif), also known as neutrophil-activating peptide (NAP)/IL-8 family, exert pro-inflammatory activity mainly through their action on neutrophils (e.g., IL-8 and NAP-2), whereas members of the "C-C branch" family appear to attract certain mononuclear cells. Members of the "C-C branch" include PF4, MIPs, MCPs, and the chemokine polypeptides of the present invention.

Numerous biological activities have been assigned to this chemokine family. The macrophage inflammatory protein 1α and 1β are chemotactic for distinct lymphocyte populations and monocytes (Schall, T.J., Cytokine, 3:165 (1991)), while MCP-1 has been described as a specific monocyte chemoattractant (Matsushima, K., et al., J. Exp. Med., 169:1485 (1989)). The common function of this chemokine family is their ability to stimulate chemotactic migration of distinct sets of cells, for example, immune cells (leukocytes) and fibroblasts. These chemokines are also able to activate certain cells in this family.

The immune cells which are responsive to the chemokines have a vast number of *in vivo* functions and therefore their regulation by such chemokines is an important area in the treatment of disease.

For example, eosinophils destroy parasites to lessen parasitic infection. Eosinophils are also responsible for chronic inflammation in the airways of the respiratory system. Macrophages are responsible for suppressing tumor formation in vertebrates. Further, basophils release histamine which may play an important role in allergic inflammation. Accordingly, promoting and inhibiting such cells, has wide therapeutic application.

In accordance with one aspect of the present invention, there are provided novel polypeptides which are Ckβ-9 as well as fragments, analogs and derivatives thereof. The polypeptides of the present invention are of human origin.

In accordance with another aspect of the present invention, there are provided polynucleotides (DNA or RNA) which encode such polypeptides.

In accordance with yet a further aspect of the present invention, there is provided a process for producing such polypeptides by recombinant techniques.

In accordance with yet a further aspect of the present invention, there is provided a process for utilizing such

polypeptides, or polynucleotides encoding such polypeptides for therapeutic purposes, for example, to treat solid tumors, chronic infections, auto-immune diseases, psoriasis, asthma, allergy, to regulate hematopoiesis, and to promote wound healing.

In accordance with yet a further aspect of the present invention, there are provided antibodies against such polypeptides.

In accordance with yet another aspect of the present invention, there are provided antagonist/inhibitors to such polypeptides, which may be used to inhibit the action of such polypeptides, for example, in the treatment of auto-immune diseases, chronic inflammatory and infective diseases, histamine-mediated allergic reactions, prostaglandin-independent fever, bone marrow failure, silicosis, sarcoidosis, hyper-eosinophilic syndrome and lung inflammation.

These and other aspects of the present invention should be apparent to those skilled in the art from the teachings herein.

The following drawings are illustrative of embodiments of the invention and are not meant to limit the scope of the invention as encompassed by the claims.

Figure 1 displays the cDNA sequence and corresponding deduced amino acid sequence of Ckβ-9. The initial 22 amino acids represent the leader sequence such that the putative mature polypeptide comprises 102 amino acids. The standard one-letter abbreviation for amino acids is used.

Figure 2 displays the amino acid sequence homology between Ckβ-9 and the mature peptide of eotaxin (bottom).

In accordance with an aspect of the present invention, there are provided isolated nucleic acids (polynucleotides) which encode for the mature polypeptides having the deduced amino acid sequences of Figure 1 or for the mature

polypeptide encoded by the cDNA of the clones deposited as ATCC Deposit No. 75803 on June 7, 1994.

The polynucleotide encoding Ckβ-9 was discovered in a cDNA library derived from a human breast lymph node. Ckβ-9 is structurally related to the chemokine family. It contains an open reading frame encoding a protein of 125 amino acid residues of which approximately the first 23 amino acids residues are the putative leader sequence such that the mature protein comprises 102 amino acids. The protein exhibits the highest degree of homology to eotaxin with 32% identity and 47% similarity over the entire coding sequence. It is also important that the four spatially conserved cysteine residues in chemokines are found in the polypeptides of the present invention.

The polynucleotides of the present invention may be in the form of RNA or in the form of DNA, which DNA includes cDNA, genomic DNA, and synthetic DNA. The DNA may be double-stranded or single-stranded, and if single stranded may be the coding strand or non-coding (anti-sense) strand. The coding sequence which encodes the mature polypeptides may be identical to the coding sequence shown in Figure 1 or that of the deposited clones or may be a different coding sequence which coding sequence, as a result of the redundancy or degeneracy of the genetic code, encodes the same mature polypeptides as the DNA of Figure 1 or the deposited cDNA.

The polynucleotides which encodes for the mature polypeptides of Figure 1 or for the mature polypeptides encoded by the deposited cDNA may include: only the coding sequence for the mature polypeptide; the coding sequence for the mature polypeptide and additional coding sequence such as a leader or secretory sequence or a proprotein sequence; the coding sequence for the mature polypeptide (and optionally additional coding sequence) and non-coding sequence, such as introns or non-coding sequence 5' and/or 3' of the coding sequence for the mature polypeptides.

Thus, the term "polynucleotide encoding a polypeptide" encompasses a polynucleotide which includes only coding sequence for the polypeptide as well as a polynucleotide which includes additional coding and/or non-coding sequence.

The present invention further relates to variants of the hereinabove described polynucleotides which encode for fragments, analogs and derivatives of the polypeptide having the deduced amino acid sequence of Figure 1 or the polypeptide encoded by the cDNA of the deposited clones. The variant of the polynucleotides may be a naturally occurring allelic variant of the polynucleotides or a non-naturally occurring variant of the polynucleotides.

Thus, the present invention includes polynucleotides encoding the same mature polypeptides as shown in Figure 1 or the same mature polypeptides encoded by the cDNA of the deposited clones as well as variants of such polynucleotides which variants encode for a fragment, derivative or analog of the polypeptides of Figure 1 or the polypeptides encoded by the cDNA of the deposited clones. Such nucleotide variants include deletion variants, substitution variants and addition or insertion variants.

As hereinabove indicated, the polynucleotides may have a coding sequence which is a naturally occurring allelic variant of the coding sequence shown in Figure 1 or of the coding sequence of the deposited clones. As known in the art, an allelic variant is an alternate form of a polynucleotide sequence which may have a substitution, deletion or addition of one or more nucleotides, which does not substantially alter the function of the encoded polypeptide.

The present invention also includes polynucleotides, wherein the coding sequence for the mature polypeptides may be fused in the same reading frame to a polynucleotide sequence which aids in expression and secretion of a polypeptide from a host cell, for example, a leader sequence

which functions as a secretory sequence for controlling transport of a polypeptide from the cell. The polypeptide having a leader sequence is a preprotein and may have the leader sequence cleaved by the host cell to form the mature form of the polypeptide. The polynucleotides may also encode for a proprotein which is the mature protein plus additional 5' amino acid residues. A mature protein having a prosequence is a proprotein and is an inactive form of the protein. Once the prosequence is cleaved an active mature protein remains.

Thus, for example, the polynucleotide of the present invention may encode for a mature protein, or for a protein having a prosequence or for a protein having both a prosequence and a presequence (leader sequence).

The polynucleotides of the present invention may also have the coding sequence fused in frame to a marker sequence which allows for purification of the polypeptides of the present invention. The marker sequence may be a hexa-histidine tag supplied by a pQE-9 vector to provide for purification of the mature polypeptides fused to the marker in the case of a bacterial host, or, for example, the marker sequence may be a hemagglutinin (HA) tag when a mammalian host, e.g. COS-7 cells, is used. The HA tag corresponds to an epitope derived from the influenza hemagglutinin protein (Wilson, I., et al., Cell, 37:767 (1984)).

The present invention further relates to polynucleotides which hybridize to the hereinabove-described sequences if there is at least 50% and preferably 70% identity between the sequences. The present invention particularly relates to polynucleotides which hybridize under stringent conditions to the hereinabove-described polynucleotides. As herein used, the term "stringent conditions" means hybridization will occur only if there is at least 95% and preferably at least 97% identity between the sequences. The polynucleotides which hybridize to the

hereinabove described polynucleotides in a preferred embodiment encode polypeptides which retain substantially the same biological function or activity as the mature polypeptide encoded by the cDNA of Figure 1 or the deposited cDNA.

The deposit(s) referred to herein will be maintained under the terms of the Budapest Treaty on the International Recognition of the Deposit of Micro-organisms for purposes of Patent Procedure. These deposits are provided merely as convenience to those of skill in the art and are not an admission that a deposit is required under 35 U.S.C. §112. The sequence of the polynucleotides contained in the deposited materials, as well as the amino acid sequence of the polypeptides encoded thereby, are incorporated herein by reference and are controlling in the event of any conflict with any description of sequences herein. A license may be required to make, use or sell the deposited materials, and no such license is hereby granted.

The present invention further relates to chemokine polypeptides which have the deduced amino acid sequences of Figure 1 or which has the amino acid sequence encoded by the deposited cDNA, as well as fragments, analogs and derivatives of such polypeptides.

The terms "fragment," "derivative" and "analog" when referring to the polypeptides of Figure 1 or that encoded by the deposited cDNA, means polypeptides which retain essentially the same biological function or activity as such polypeptides. Thus, an analog includes a proprotein which can be activated by cleavage of the proprotein portion to produce an active mature polypeptide.

The chemokine polypeptides of the present invention may be recombinant polypeptides, natural polypeptides or a synthetic polypeptides, preferably recombinant polypeptides.

The fragment, derivative or analog of the polypeptides of Figure 1 or that encoded by the deposited cDNA may be (i)

one in which one or more of the amino acid residues are substituted with a conserved or non-conserved amino acid residue (preferably a conserved amino acid residue) and such substituted amino acid residue may or may not be one encoded by the genetic code, or (ii) one in which one or more of the amino acid residues includes a substituent group, or (iii) one in which the mature polypeptide is fused with another compound, such as a compound to increase the half-life of the polypeptide (for example, polyethylene glycol), or (iv) one in which the additional amino acids are fused to the mature polypeptide, such as a leader or secretory sequence or a sequence which is employed for purification of the mature polypeptide or a proprotein sequence. Such fragments, derivatives and analogs are deemed to be within the scope of those skilled in the art from the teachings herein.

The polypeptides and polynucleotides of the present invention are preferably provided in an isolated form, and preferably are purified to homogeneity.

The term "isolated" means that the material is removed from its original environment (e.g., the natural environment if it is naturally occurring). For example, a naturally-occurring polynucleotide or polypeptide present in a living animal is not isolated, but the same polynucleotide or polypeptide, separated from some or all of the coexisting materials in the natural system, is isolated. Such polynucleotides could be part of a vector and/or such polynucleotides or polypeptides could be part of a composition, and still be isolated in that such vector or composition is not part of its natural environment.

The present invention also relates to vectors which include polynucleotides of the present invention, host cells which are genetically engineered with vectors of the invention and the production of polypeptides of the invention by recombinant techniques.

Host cells are genetically engineered (transduced or transformed or transfected) with the vectors of this invention which may be, for example, a cloning vector or an expression vector. The vector may be, for example, in the form of a plasmid, a viral particle, a phage, etc. The engineered host cells can be cultured in conventional nutrient media modified as appropriate for activating promoters, selecting transformants or amplifying the Ckβ-9 genes. The culture conditions, such as temperature, pH and the like, are those previously used with the host cell selected for expression, and will be apparent to the ordinarily skilled artisan.

The polynucleotides of the present invention may be employed for producing polypeptides by recombinant techniques. Thus, for example, the polynucleotide may be included in any one of a variety of expression vectors for expressing a polypeptide. Such vectors include chromosomal, nonchromosomal and synthetic DNA sequences, e.g., derivatives of SV40; bacterial plasmids; phage DNA; baculovirus; yeast plasmids; vectors derived from combinations of plasmids and phage DNA, viral DNA such as vaccinia, adenovirus, fowl pox virus, and pseudorabies. However, any other vector may be used as long as it is replicable and viable in the host.

The appropriate DNA sequence may be inserted into the vector by a variety of procedures. In general, the DNA sequence is inserted into an appropriate restriction endonuclease site(s) by procedures known in the art. Such procedures and others are deemed to be within the scope of those skilled in the art.

The DNA sequence in the expression vector is operatively linked to an appropriate expression control sequence(s) (promoter) to direct mRNA synthesis. As representative examples of such promoters, there may be mentioned: LTR or SV40 promoter, the E. coli. lac or trp, the phage lambda P.

promoter and other promoters known to control expression of genes in prokaryotic or eukaryotic cells or their viruses. The expression vector also contains a ribosome binding site for translation initiation and a transcription terminator. The vector may also include appropriate sequences for amplifying expression.

In addition, the expression vectors preferably contain one or more selectable marker genes to provide a phenotypic trait for selection of transformed host cells such as dihydrofolate reductase or neomycin resistance for eukaryotic cell culture, or such as tetracycline or ampicillin resistance in E. coli.

The vector containing the appropriate DNA sequence as hereinabove described, as well as an appropriate promoter or control sequence, may be employed to transform an appropriate host to permit the host to express the protein.

As representative examples of appropriate hosts, there may be mentioned: bacterial cells, such as E. coli, Streptomyces, Salmonella typhimurium; fungal cells, such as yeast; insect cells such as Drosophila and Sf9; animal cells such as CHO, COS or Bowes melanoma; plant cells, etc. The selection of an appropriate host is deemed to be within the scope of those skilled in the art from the teachings herein.

More particularly, the present invention also includes recombinant constructs comprising one or more of the sequences as broadly described above. The constructs comprise a vector, such as a plasmid or viral vector, into which a sequence of the invention has been inserted, in a forward or reverse orientation. In a preferred aspect of this embodiment, the construct further comprises regulatory sequences, including, for example, a promoter, operably linked to the sequence. Large numbers of suitable vectors and promoters are known to those of skill in the art, and are commercially available. The following vectors are provided by way of example. Bacterial: pQE70, pQE60, pQE-9 (Qiagen),

pBS, pD10, phagescript, psiX174, pBluescript SK, pBSKS, pNH8A, pNH16a, pNH18A, pNH46A (Stratagene); ptrc99a, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia). Eukaryotic: pWLNEO, pSV2CAT, pOG44, pXT1, pSG (Stratagene) pSVK3, pBPV, pMSG, pSVL (Pharmacia). However, any other plasmid or vector may be used as long as they are replicable and viable in the host.

Promoter regions can be selected from any desired gene using CAT (chloramphenicol transferase) vectors or other vectors with selectable markers. Two appropriate vectors are pKK232-8 and pCM7. Particular named bacterial promoters include lacI, lacZ, T3, T7, gpt, lambda P_R, P_L and trp. Eukaryotic promoters include CMV immediate early, HSV thymidine kinase, early and late SV40, LTRs from retrovirus, and mouse metallothionein-I. Selection of the appropriate vector and promoter is well within the level of ordinary skill in the art.

In a further embodiment, the present invention relates to host cells containing the above-described constructs. The host cell can be a higher eukaryotic cell, such as a mammalian cell, or a lower eukaryotic cell, such as a yeast cell, or the host cell can be a prokaryotic cell, such as a bacterial cell. Introduction of the construct into the host cell can be effected by calcium phosphate transfection, DEAE-Dextran mediated transfection, or electroporation. (Davis, L., Dibner, M., Battey, I., Basic Methods in Molecular Biology, (1986)).

The constructs in host cells can be used in a conventional manner to produce the gene product encoded by the recombinant sequence. Alternatively, the polypeptides of the invention can be synthetically produced by conventional peptide synthesizers.

Mature proteins can be expressed in mammalian cells, yeast, bacteria, or other cells under the control of appropriate promoters. Cell-free translation systems can

also be employed to produce such proteins using RNAs derived from the DNA constructs of the present invention. Appropriate cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described by Sambrook, et al., Molecular Cloning: A Laboratory Manual, Second Edition, Cold Spring Harbor, N.Y., (1989), the disclosure of which is hereby incorporated by reference.

Transcription of the DNA encoding the polypeptides of the present invention by higher eukaryotes is increased by inserting an enhancer sequence into the vector. Enhancers are cis-acting elements of DNA, usually about from 10 to 300 bp that act on a promoter to increase its transcription. Examples including the SV40 enhancer on the late side of the replication origin bp 100 to 270, a cytomegalovirus early promoter enhancer, the polyoma enhancer on the late side of the replication origin, and adenovirus enhancers.

Generally, recombinant expression vectors will include origins of replication and selectable markers permitting transformation of the host cell, e.g., the ampicillin resistance gene of E. coli and S. cerevisiae TRP1 gene, and a promoter derived from a highly-expressed gene to direct transcription of a downstream structural sequence. Such promoters can be derived from operons encoding glycolytic enzymes such as 3-phosphoglycerate kinase (PGK), α-factor, acid phosphatase, or heat shock proteins, among others. The heterologous structural sequence is assembled in appropriate phase with translation initiation and termination sequences, and preferably, a leader sequence capable of directing secretion of translated protein into the periplasmic space or extracellular medium. Optionally, the heterologous sequence can encode a fusion protein including an N-terminal identification peptide imparting desired characteristics, e.g., stabilization or simplified purification of expressed recombinant product.

Useful expression vectors for bacterial use are constructed by inserting a structural DNA sequence encoding a desired protein together with suitable translation initiation and termination signals in operable reading phase with a functional promoter. The vector will comprise one or more phenotypic selectable markers and an origin of replication to ensure maintenance of the vector and to, if desirable, provide amplification within the host. Suitable prokaryotic hosts for transformation include E. coli, Bacillus subtilis, Salmonella typhimurium and various species within the genera Pseudomonas, Streptomyces, and Staphylococcus, although others may also be employed as a matter of choice.

As a representative but nonlimiting example, useful expression vectors for bacterial use can comprise a selectable marker and bacterial origin of replication derived from commercially available plasmids comprising genetic elements of the well known cloning vector pBR322 (ATCC 37017). Such commercial vectors include, for example, pKK223-3 (Pharmacia Fine Chemicals, Uppsala, Sweden) and pGEM1 (Promega Biotec, Madison, WI, USA). These pBR322 "backbone" sections are combined with an appropriate promoter and the structural sequence to be expressed.

Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter is induced by appropriate means (e.g., temperature shift or chemical induction) and cells are cultured for an additional period.

Cells are typically harvested by centrifugation, disrupted by physical or chemical means, and the resulting crude extract retained for further purification.

Microbial cells employed in expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell

lysing agents, such methods are well know to those skilled in the art.

Various mammalian cell culture systems can also be employed to express recombinant protein. Examples of mammalian expression systems include the COS-7 lines of monkey kidney fibroblasts, described by Gluzman, Cell, 23:175 (1981), and other cell lines capable of expressing a compatible vector, for example, the C127, 3T3, CHO, HeLa and BHK cell lines. Mammalian expression vectors will comprise an origin of replication, a suitable promoter and enhancer, and also any necessary ribosome binding sites, polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences, and 5' flanking nontranscribed sequences. DNA sequences derived from the SV40 splice, and polyadenylation sites may be used to provide the required nontranscribed genetic elements.

The chemokine polypeptides can be recovered and purified from recombinant cell cultures by methods including ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography hydroxylapatite chromatography and lectin chromatography. Protein refolding steps can be used, as necessary, in completing configuration of the mature protein. Finally, high performance liquid chromatography (HPLC) can be employed for final purification steps.

The chemokine polypeptides of the present invention may be a naturally purified product, or a product of chemical synthetic procedures, or produced by recombinant techniques from a prokaryotic or eukaryotic host (for example, by bacterial, yeast, higher plant, insect and mammalian cells in culture). Depending upon the host employed in a recombinant production procedure, the polypeptides of the present invention may be glycosylated or may be non-glycosylated.

Polypeptides of the invention may also include an initial methionine amino acid residue.

The chemokine polypeptides may be used to inhibit bone marrow stem cell colony formation as adjunct protective treatment during cancer chemotherapy and for leukemia.

The chemokine polypeptides may also be used to inhibit epidermal keratinocyte proliferation for treatment of psoriasis, which is characterized by keratinocyte hyper-proliferation.

The chemokine polypeptides may also be used to treat solid tumors by stimulating the invasion and activation of host defense cells, e.g., cytotoxic T cells and macrophages. They may also be used to enhance host defenses against resistant chronic infections, for example, mycobacterial infections via the attraction and activation of microbicidal leukocytes.

The chemokine polypeptides may also be used to treat auto-immune disease and lymphocytic leukemia by inhibiting T cell proliferation by the inhibition of IL2 biosynthesis.

Ckβ-9 may also be used in wound healing, both via the recruitment of debris clearing and connective tissue promoting inflammatory cells and also via its control of excessive TGFβ-mediated fibrosis. In this same manner, Ckβ-9 may also be used to treat other fibrotic disorders, including liver cirrhosis, osteoarthritis and pulmonary fibrosis. The chemokine polypeptides also increase the presence of eosinophils which have the distinctive function of killing the larvae of parasites that invade tissues, as in schistosomiasis, trichinosis and ascariasis. They may also be used to regulate hematopoiesis, by regulating the activation and differentiation of various hematopoietic progenitor cells .

Chemokines may also be employed as inhibitors of angiogenesis, therefore, they have anti-tumor effects.

The chemokine polypeptides of the present invention are also useful for identifying other molecules which have similar biological activity. An example of a screen for this is isolating the coding region of the genes by using the known DNA sequence to synthesize oligonucleotide probes. Labeled oligonucleotides having a sequence complementary to that of the genes of the present invention are used to screen a library of human cDNA, genomic DNA or mRNA to determine which members of the library the probe hybridizes to.

The present invention also relates to a diagnostic assays for detecting altered levels of the polypeptides or the mRNA which provides the message for such polypeptides, both quantitatively and qualitatively. Such assays are well-known in the art and include an ELISA assay, the radioimmunoassay and RT-PCR. The levels of the polypeptides, or their mRNAs, which are detected in the assays may be employed for the elucidation of the significance of the polypeptides in various diseases and for the diagnosis of diseases in which altered levels of the polypeptides may be significant.

This invention provides a method for identification of the receptors for the polypeptides. The gene encoding the receptors can be identified by expression cloning. Polyadenylated RNA is prepared from a cell responsive to the polypeptides, and a cDNA library created from this RNA is divided into pools and used to transfect COS cells or other cells that are not responsive to the polypeptides. Transfected cells which are grown on glass slides are exposed to the labeled polypeptides. The polypeptides can be labeled by a variety of means including iodination or inclusion of a recognition site for a site-specific protein kinase. Following fixation and incubation, the slides are subjected to autoradiographic analysis. Positive pools are identified and sub-pools are prepared and retransfected using an iterative sub-pooling and rescreening process, eventually

yielding a single clones that encodes the putative receptor. As an alternative approach for receptor identification, the labeled polypeptides can be photoaffinity linked with cell membrane or extract preparations that express the receptor molecule. Cross-linked material is resolved by PAGE analysis and exposed to x-ray film. The labeled complex containing the receptors of the polypeptides can be excised, resolved into peptide fragments, and subjected to protein microsequencing. The amino acid sequence obtained from microsequencing would be used to design a set of generate oligonucleotide probes to screen a cDNA library to identify the genes encoding the putative receptors.

This invention provides a method of screening drugs to identify those which enhance (agonists) or block (antagonists) interaction of the polypeptides to their identified receptors. An agonist is a compound which increases the natural biological functions of the polypeptides, while antagonists eliminate such functions. As an example, a mammalian cell or membrane preparation expressing the receptors of the polypeptides would be incubated with a labeled chemokine polypeptide, eg. radioactivity, in the presence of the drug. The ability of the drug to enhance or block this interaction could then be measured.

Potential antagonists include antibodies, or in some cases, oligonucleotides, which bind to the polypeptides. Another example of a potential antagonist is a negative dominant mutant of the polypeptides. Negative dominant mutants are polypeptides which bind to the receptor of the wild-type polypeptide, but fail to retain biological activity.

An assay to detect negative dominant mutants of the polypeptides include an *in vitro* chemotaxis assay wherein a multiwell chemotaxis chamber equipped with polyvinylpyrrolidone-free polycarbonate membranes is used to

measure the chemoattractant ability of the polypeptides for leukocytes in the presence and absence of potential antagonist/inhibitor or agonist molecules.

Antisense constructs prepared using antisense technology are also potential antagonists. Antisense technology can be used to control gene expression through triple-helix formation or antisense DNA or RNA, both of which methods are based on binding of a polynucleotide to DNA or RNA. For example, the 5' coding portion of the polynucleotide sequence, which encodes for the mature polypeptides of the present invention, is used to design an antisense RNA oligonucleotide of from about 10 to 40 base pairs in length. A DNA oligonucleotide is designed to be complementary to a region of the gene involved in transcription (triple- helix, see Lee et al., Nucl. Acids Res., 6:3073 (1979); Cooney et al, Science, 241:456 (1988); and Dervan et al., Science, 251: 1360 (1991)), thereby preventing transcription and the production of the polypeptides. The antisense RNA oligonucleotide hybridizes to the mRNA *in vivo* and blocks translation of the mRNA molecule into the polypeptides (antisense - Okano, J. Neurochem., 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). The oligonucleotides described above can also be delivered to cells such that the antisense RNA or DNA may be expressed *in vivo* to inhibit production of the polypeptides.

Another potential antagonist is a peptide derivative of the polypeptides which are naturally or synthetically modified analogs of the polypeptides that have lost biological function yet still recognize and bind to the receptors of the polypeptides to thereby effectively block the receptors. Examples of peptide derivatives include, but are not limited to, small peptides or peptide-like molecules.

The antagonists may be employed to inhibit the chemotaxis and activation of macrophages and their

precursors, and of neutrophils, basophils, B lymphocytes and some T cell subsets, e.g., activated and CD8 cytotoxic T cells and natural killer cells, in auto-immune and chronic inflammatory and infective diseases. Examples of auto-immune diseases include rheumatoid arthritis, multiple sclerosis, and insulin-dependent diabetes. Some infectious diseases include silicosis, sarcoidosis, idiopathic pulmonary fibrosis by preventing the recruitment and activation of mononuclear phagocytes, idiopathic hyper-eosinophilic syndrome by preventing eosinophil production and migration, endotoxic shock by preventing the migration of macrophages and their production of the chemokine polypeptides of the present invention. The antagonists may also be used for treating atherosclerosis, by preventing monocyte infiltration in the artery wall.

The antagonists may also be used to treat histamine-mediated allergic reactions by inhibiting chemokine-induced mast cell and basophil degranulation and release of histamine.

The antagonists may also be used to treat inflammation by preventing the attraction of monocytes to a wound area. They may also be used to regulate normal pulmonary macrophage populations, since acute and chronic inflammatory pulmonary diseases are associated with sequestration of mononuclear phagocytes in the lung.

Antagonists may also be used to treat rheumatoid arthritis by preventing the attraction of monocytes into synovial fluid in the joints of patients. Monocyte influx and activation plays a significant role in the pathogenesis of both degenerative and inflammatory arthropathies.

The antagonists may be used to interfere with the deleterious cascades attributed primarily to IL-1 and TNF, which prevents the biosynthesis of other inflammatory cytokines. In this way, the antagonists may be used to prevent inflammation. The antagonists may also be used to

inhibit prostaglandin-independent fever induced by chemokines.

The antagonists may also be used to treat cases of bone marrow failure, for example, aplastic anemia and myelodysplastic syndrome.

The antagonists may also be used to treat asthma and allergy by preventing eosinophil accumulation in the lung. The antagonists may be employed in a composition with a pharmaceutically acceptable carrier, e.g., as hereinafter described.

The chemokine polypeptides of the present invention may be employed in combination with a suitable pharmaceutical carrier. Such compositions comprise a therapeutically effective amount of the polypeptide, and a pharmaceutically acceptable carrier or excipient. Such a carrier includes but is not limited to saline, buffered saline, dextrose, water, glycerol, ethanol, and combinations thereof. The formulation should suit the mode of administration.

The invention also provides a pharmaceutical pack or kit comprising one or more containers filled with one or more of the ingredients of the pharmaceutical compositions of the invention. Associated with such container(s) can be a notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, which notice reflects approval by the agency of manufacture, use or sale for human administration. In addition, the polypeptides of the present invention may be employed in conjunction with other therapeutic compounds.

The pharmaceutical compositions may be administered in a convenient manner such as by the topical, intravenous, intraperitoneal, intramuscular, intratumor, subcutaneous, intranasal or intradermal routes. The polypeptides are administered in an amount which is effective for treating and/or prophylaxis of the specific indication. In general, the polypept-- will be administered in an amount of at

least about 10 μg/kg body weight and in most cases they will be administered in an amount not in excess of about 8 mg/Kg body weight per day. In most cases, the dosage is from about 10 μg/kg to about 1 mg/kg body weight daily, taking into account the routes of administration, symptoms, etc.

The chemokine polypeptides, and agonists or antagonists which are polypeptides, may be employed in accordance with the present invention by expression of such polypeptides in vivo, which is often referred to as "gene therapy."

Thus, for example, cells from a patient may be engineered with a polynucleotide (DNA or RNA) encoding a polypeptide *ex vivo*, with the engineered cells then being provided to a patient to be treated with the polypeptide. Such methods are well-known in the art. For example, cells may be engineered by procedures known in the art by use of a retroviral particle containing RNA encoding a polypeptide of the present invention.

Similarly, cells may be engineered *in vivo* for expression of a polypeptide *in vivo* by, for example, procedures known in the art. As known in the art, a producer cell for producing a retroviral particle containing RNA encoding the polypeptide of the present invention may be administered to a patient for engineering cells *in vivo* and expression of the polypeptide *in vivo*. These and other methods for administering a polypeptide of the present invention by such method should be apparent to those skilled in the art from the teachings of the present invention. For example, the expression vehicle for engineering cells may be other than a retrovirus, for example, an adenovirus which may be used to engineer cells in vivo after combination with a suitable delivery vehicle.

The sequences of the present invention are also valuable for chromosome identification. The sequence is specifically targeted to and can hybridize with a particular location on an individual human chromosome. Moreover, there is a current

need for identifying particular sites on the chromosome. Few chromosome marking reagents based on actual sequence data (repeat polymorphisms) are presently available for marking chromosomal location. The mapping of DNAs to chromosomes according to the present invention is an important first step in correlating those sequences with genes associated with disease.

Briefly, sequences can be mapped to chromosomes by preparing PCR primers (preferably 15-25 bp) from the cDNA. Computer analysis of the cDNA is used to rapidly select primers that do not span more than one exon in the genomic DNA, thus complicating the amplification process. These primers are then used for PCR screening of somatic cell hybrids containing individual human chromosomes. Only those hybrids containing the human gene corresponding to the primer will yield an amplified fragment.

PCR mapping of somatic cell hybrids is a rapid procedure for assigning a particular DNA to a particular chromosome. Using the present invention with the same oligonucleotide primers, sublocalization can be achieved with panels of fragments from specific chromosomes or pools of large genomic clones in an analogous manner. Other mapping strategies that can similarly be used to map to its chromosome include *in situ* hybridization, prescreening with labeled flow-sorted chromosomes and preselection by hybridization to construct chromosome specific-cDNA libraries.

Fluorescence *in situ* hybridization (FISH) of a cDNA clones to a metaphase chromosomal spread can be used to provide a precise chromosomal location in one step. This technique can be used with cDNA as short as 500 or 600 bases; however, clones larger than 2,000 bp have a higher likelihood of binding to a unique chromosomal location with sufficient signal intensity for simple detection. FISH requires use of the clones from which the EST was derived, and the longer the better. For example, 2,000 bp is good, 4,600 is better, and

more than 4,000 is probably not necessary to get good results a reasonable percentage of the time. For a review of this technique, see Verma et al., Human Chromosomes: a Manual of Basic Techniques, Pergamon Press, New York (1988).

Once a sequence has been mapped to a precise chromosomal location, the physical position of the sequence on the chromosome can be correlated with genetic map data. Such data are found, for example, in V. McKusick, Mendelian Inheritance in Man (available on line through Johns Hopkins University Welch Medical Library). The relationship between genes and diseases that have been mapped to the same chromosomal region are then identified through linkage analysis (coinheritance of physically adjacent genes).

Next, it is necessary to determine the differences in the cDNA or genomic sequence between affected and unaffected individuals. If a mutation is observed in some or all of the affected individuals but not in any normal individuals, then the mutation is likely to be the causative agent of the disease.

With current resolution of physical mapping and genetic mapping techniques, a cDNA precisely localized to a chromosomal region associated with the disease could be one of between 50 and 500 potential causative genes. (This assumes 1 megabase mapping resolution and one gene per 20 kb).

The polypeptides, their fragments or other derivatives, or analogs thereof, or cells expressing them can be used as an immunogen to produce antibodies thereto. These antibodies can be, for example, polyclonal or monoclonal antibodies. The present invention also includes chimeric, single chain, and humanized antibodies, as well as Fab fragments, or the product of an Fab expression library. Various procedures known in the art may be used for the production of such antibodies and fragments.

Antibodies generated against the polypeptides corresponding to a sequence of the present invention can be obtained by direct injection of the polypeptides into an animal or by administering the polypeptides to an animal, preferably a nonhuman. The antibody so obtained will then bind the polypeptides itself. In this manner, even a sequence encoding only a fragment of the polypeptides can be used to generate antibodies binding the whole native polypeptides. Such antibodies can then be used to isolate the polypeptide from tissue expressing that polypeptide.

For preparation of monoclonal antibodies, any technique which provides antibodies produced by continuous cell line cultures can be used. Examples include the hybridoma technique (Kohler and Milstein, 1975, Nature, 256:495-497), the trioma technique, the human B-cell hybridoma technique (Kozbor et al., 1983, Immunology Today 4:72), and the EBV-hybridoma technique to produce human monoclonal antibodies (Cole, et al., 1985, in Monoclonal Antibodies and Cancer Therapy, Alan R. Liss, Inc., pp. 77-96).

Techniques described for the production of single chain antibodies (U.S. Patent 4,946,778) can be adapted to produce single chain antibodies to immunogenic polypeptide products of this invention.

The present invention will be further described with reference to the following examples; however, it is to be understood that the present invention is not limited to such examples. All parts or amounts, unless otherwise specified, are by weight.

In order to facilitate understanding of the following examples certain frequently occurring methods and/or terms will be described.

"Plasmids" are designated by a lower case p preceded and/or followed by capital letters and/or numbers. The starting plasmids herein are either commercially available, publicly available on an unrestricted basis, or can be

constructed from available plasmids in accord with published procedures. In addition, equivalent plasmids to those described are known in the art and will be apparent to the ordinarily skilled artisan.

"Digestion" of DNA refers to catalytic cleavage of the DNA with a restriction enzyme that acts only at certain sequences in the DNA. The various restriction enzymes used herein are commercially available and their reaction conditions, cofactors and other requirements were used as would be known to the ordinarily skilled artisan. For analytical purposes, typically 1 µg of plasmid or DNA fragment is used with about 2 units of enzyme in about 20 µl of buffer solution. For the purpose of isolating DNA fragments for plasmid construction, typically 5 to 50 µg of DNA are digested with 20 to 250 units of enzyme in a larger volume. Appropriate buffers and substrate amounts for particular restriction enzymes are specified by the manufacturer. Incubation times of about 1 hour at 37°C are ordinarily used, but may vary in accordance with the supplier's instructions. After digestion the reaction is electrophoresed directly on a polyacrylamide gel to isolate the desired fragment.

Size separation of the cleaved fragments is performed using 8 percent polyacrylamide gel described by Goeddel, D. et al., Nucleic Acids Res., 8:4057 (1980).

"Oligonucleotides" refers to either a single stranded polydeoxynucleotide or two complementary polydeoxynucleotide strands which may be chemically synthesized. Such synthetic oligonucleotides have no 5' phosphate and thus will not ligate to another oligonucleotide without adding a phosphate with an ATP in the presence of a kinase. A synthetic oligonucleotide will ligate to a fragment that has not been dephosphorylated.

"Ligation" refers to the process of forming phosphodiester bonds between two double stranded nucleic acid

fragments (Maniatis, T., et al., Id., p. 146). Unless otherwise provided, ligation may be accomplished using known buffers and conditions with 10 units to T4 DNA ligase ("ligase") per 0.5 μg of approximately equimolar amounts of the DNA fragments to be ligated.

Unless otherwise stated, transformation was performed as described in the method of Graham, F. and Van der Eb, A., Virology, 52:456-457 (1973).

Example 1

Bacterial Expression and Purification of Ckβ-9

The DNA sequence encoding for Ckβ-9, ATCC # 75803, is initially amplified using PCR oligonucleotide primers corresponding to the 5' and 3' sequences of the processed Ckβ-4 protein (minus the putative signal peptide sequence). Additional nucleotides corresponding to Ckβ-9 were added to the 5' and 3' sequences respectively. The 5' oligonucleotide primer has the sequence 5' CCC**GCATGC**GTGATGGAGGGGGCTCAG 3' contains a SphI restriction enzyme site (bold) followed by 17 nucleotides of Ckβ-9 coding sequence (underlined) starting from the second nucleotide of the sequences coding for the mature protein. The ATG codon is included in the SphI site. In the next codon following the ATG, the first base is from the SphI site and the remaining two bases correspond to the second and third base of the first codon (residue S_{34}) of the putative mature protein. As a consequence, the first base in this codon is changed from A to C comparing with the original sequences, resulting in an S to R substitution in the recombinant protein. The 3' sequence 5' **AAAGGATCC**GTCCTCTTGCAGCCTTTGG 3' contains complementary sequences to a BamHI site (bold) and is followed by 19 nucleotides of gene specific sequences preceding the termination codon. The restriction enzyme sites correspond to the restriction enzyme sites on the bacterial expression vector pQE-70 (Qiagen, Inc. 9259 Eton Avenue, Chatsworth, CA,

91311). pQE-70 encodes antibiotic resistance (Amp^r), a bacterial origin of replication (ori), an IPTG-regulatable promoter operator (P/O), a ribosome binding site (RBS), a 6-His tag and restriction enzyme sites. pQE-70 was then digested with SphI and BamHI. The amplified sequences were ligated into pQE-9 and were inserted in frame with the sequence encoding for the histidine tag and the RBS. Figure 9 shows a schematic representation of this arrangement. The ligation mixture was then used to transform the E. coli strain available from Qiagen under the trademark M15/rep 4 by the procedure described in Sambrook, J. et al., Molecular Cloning: A Laboratory Manual, Cold Spring Laboratory Press, (1989). M15/rep4 contains multiple copies of the plasmid pREP4, which expresses the lacI repressor and also confers kanamycin resistance (Kan^r). Transformants are identified by their ability to grow on LB plates and ampicillin/kanamycin resistant colonies were selected. Plasmid DNA was isolated and confirmed by restriction analysis. Clones containing the desired constructs were grown overnight (O/N) in liquid culture in LB media supplemented with both Amp (100 ug/ml) and Kan (25 ug/ml). The O/N culture is used to inoculate a large culture at a ratio of 1:100 to 1:250. The cells were grown to an optical density 600 ($O.D.^{600}$) of between 0.4 and 0.6. IPTG ("Isopropyl-B-D-thiogalacto pyranoside") was then added to a final concentration of 1 mM. IPTG induces by inactivating the lacI repressor, clearing the P/O leading to increased gene expression. Cells were grown an extra 3 to 4 hours. Cells were then harvested by centrifugation. The cell pellet was solubilized in the chaotropic agent 6 Molar Guanidine HCl pH 5.0. After clarification, solubilized Ckβ-9 was purified from this solution by chromatography on a Nickel-Chelate column under conditions that allow for tight binding by proteins containing the 6-His tag (Hochuli, E. et al., J. Chromatography 411:177-184 (1984)). Ckβ-9 (>98% pure) was eluted from the column in 6M guanidine HCl.

Protein renaturation out of GnHCl can be accomplished by several protocols (Jaenicke, R. and Rudolph, R., Protein Structure - A Practical Approach, IRL Press, New York (1990)). Initially, step dialysis is utilized to remove the GnHCL. Alternatively, the purified protein isolated from the Ni-chelate column can be bound to a second column over which a decreasing linear GnHCL gradient is run. The protein is allowed to renature while bound to the column and is subsequently eluted with a buffer containing 250 mM Imidazole, 150 mM NaCl, 25 mM Tris-HCl pH 7.5 and 10% Glycerol. Finally, soluble protein is dialyzed against a storage buffer containing 5 mM Ammonium Bicarbonate.

Example 2

Expression of Recombinant Ckβ-9 in COS cells

The expression of plasmid, Ckβ-9 HA is derived from a vector pcDNAI/Amp (Invitrogen) containing: 1) SV40 origin of replication, 2) ampicillin resistance gene, 3) E.coli replication origin, 4) CMV promoter followed by a polylinker region, a SV40 intron and polyadenylation site. A DNA fragment encoding the entire Ckβ-9 precursor and a HA tag fused in frame to its 3' end was cloned into the polylinker region of the vector, therefore, the recombinant protein expression is directed under the CMV promoter. The HA tag correspond to an epitope derived from the influenza hemagglutinin protein as previously described (I. Wilson, H. Niman, R. Heighten, A Cherenson, M. Connolly, and R. Lerner, 1984, Cell 37, 767). The infusion of HA tag to the target protein allows easy detection of the recombinant protein with an antibody that recognizes the HA epitope.

The plasmid construction strategy is described as follows:

The DNA sequence encoding for Ckβ-9, ATTC. # 75803, was constructed by PCR on the original EST cloned using two primers: the 5' primer 5' AAAGGATCCAGACATGGCTCAGTCACT 3' contains a BamH1 site followed by 18 nucleotides of Ckβ-9 coding sequence starting from the initiation codon; the 3' sequence CGCTCTAGATCAAGCGTAGTCTGGGACGTCGTATGGGTAGTTCCCTTTAGGGGTCTG 3' contains complementary sequences to XbaI site, translation stop codon, HA tag and the last 18 nucleotides of the Ckβ-9 coding sequence (not including the stop codon). Therefore, the PCR product contains a BamH1 site, Ckβ-9 coding sequence followed by HA tag fused in frame, a translation termination stop codon next to the HA tag, and an XbaI site. The PCR amplified DNA fragment and the vector, pcDNAI/Amp, were digested with BamH1 and XbaI restriction enzyme and ligated. The ligation mixture was transformed into E. coli strain SURE (available from Stratagene Cloning Systems, 11099 North Torrey Pines Road, La Jolla, CA 92037) the transformed culture was plated on ampicillin media plates and resistant colonies were selected. Plasmid DNA was isolated from transformants and examined by restriction analysis for the presence of the correct fragment. For expression of the recombinant Ckβ-9, COS cells were transfected with the expression vector by DEAE-DEXTRAN method. (J. Sambrook, E. Fritsch, T. Maniatis, Molecular Cloning: A Laboratory Manual, Cold Spring Laboratory Press, (1989)). The expression of the Ckβ-9 HA protein was detected by radiolabelling and immunoprecipitation method. (E. Harlow, D. Lane, Antibodies: A Laboratory Manual, Cold Spring Harbor Laboratory Press, (1988)). Cells were labelled for 8 hours with ^{35}S-cysteine two days post transfection. Culture media were then collected and cells were lysed with detergent (RIPA buffer (150 mM NaCl, 1% NP-40, 0.1% SDS, 1% NP-40, 0.5% DOC, 50mM Tris, pH 7.5). (Wilson, I. et al., Id. 37:767 (1984)). Both cell lysate and culture media were precipitated with a HA

specific monoclonal antibody. Proteins precipitated were analyzed by SDS-PAGE.

Numerous modifications and variations of the present invention are possible in light of the above teachings and, therefore, within the scope of the appended claims, the invention may be practiced otherwise than as particularly described.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: LI, ET AL.

(ii) TITLE OF INVENTION: Human Chemokine Beta-9 Polypeptides

(iii) NUMBER OF SEQUENCES: 2

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI, STEWART & OLSTEIN

(B) STREET: 6 BECKER FARM ROAD

(C) CITY: ROSELAND

(D) STATE: NEW JERSEY

(E) COUNTRY: USA

(F) ZIP: 07068

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 3.5 INCH DISKETTE

(B) COMPUTER: IBM PS/2

(C) OPERATING SYSTEM: MS-DOS

(D) SOFTWARE: WORD PERFECT 5.1

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE: Submitted herewith

(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA

(A) APPLICATION NUMBER:

(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: FERRARO, GREGORY D.
(B) REGISTRATION NUMBER: 36,134
(C) REFERENCE/DOCKET NUMBER: 325800-183

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 201-994-1700
(B) TELEFAX: 201-994-1744

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 378 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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ATGGCTCAGT CACTGGCTCT GAGCCTCCTT ATCCTGGTTC TGGCCTTTGG CATCCCCAGG   60
ACCCAAGGCA CTGATGGAGC GGCTCAGGAC TGTTGCCTCA AGTACAGCCA AAGGAAGATT  120
CCCGCCAAGG TTGTCCCCAG CTACCGGAAG CACGAACCAA GCTTAGGCTC CTCCATCCCA  180
GCTATCCTCT TCTTGCCCCG CAAGCGCTCT CAGGCAGAGC TATGTCCAGA CCCAAAGCAG  240
CTCTGGCTGC AGCAGCTGAT GCAGCATCTG GACAAGACAC CATTCCCCAC AGAAACCAGC  300
CCACGGCTGC AGGAAGGACA GCCCGGCCTC CAAGACTGGC AAGAAAGGAA AGGGCTCCAA  360
AGGCTGCAAG AGGACTGA                                                378
```

-32-

(3) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 125 AMINO ACIDS

(B) TYPE: AMINO ACID

(C) STRANDEDNESS:

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
Met Ala Gln Ser Leu Ala Leu Ser Leu Leu Ile Leu Val Leu Ala
           -20                 -15                 -10
Phe Gly Ile Pro Arg Thr Gln Gly Ser Asp Gly Gly Ala Gln Asp
            -5                   1                   5
Cys Cys Leu Lys Tyr Ser Gln Arg Lys Ile Pro Ala Lys Val Val
        10                  15                  20
Arg Ser Tyr Arg Lys Gln Glu Pro Ser Leu Gly Cys Ser Ile Pro
        25                  30                  35
Ala Ile Leu Phe Leu Pro Arg Lys Arg Ser Gln Ala Glu Leu Cys
        40                  45                  50
Ala Asp Pro Lys Glu Leu Tyr Val Gln Gln Leu Met Gln His Leu
        55                  60                  65
Asp Lys Thr Pro Phe Pro Thr Glu Thr Ser Pro Gly Leu Gln Glu
        70                  75                  80
Gly Gln Gly Gly Leu Gln Asp Trp Gln Glu Arg Lys Gly Leu Gln
        85                  90                  95
Arg Leu Gln Glu Asp
       100
```

WHAT IS CLAIMED IS:

1. An isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide encoding a Ckβ-9 polypeptide having the deduced amino acid sequence of Figure 1 or a fragment, analog or derivative of said polypeptide; and

(b) a polynucleotide encoding a Ckβ-9 polypeptide having the amino acid sequence encoded by the cDNA contained in ATCC Deposit No. 75803 or a fragment, analog or derivative of said polypeptide.

2. The polynucleotide of Claim 1 wherein the polynucleotide is DNA.

3. The polynucleotide of Claim 1 wherein the polynucleotide is RNA.

4. The polynucleotide of Claim 1 wherein the polynucleotide is genomic DNA.

5. The polynucleotide of Claim 2 wherein said polynucleotide encodes Ckβ-9 having the deduced amino acid sequence of Figure 1.

6. The polynucleotide of Claim 2 wherein said polynucleotide encodes a Ckβ-9 polypeptide encoded by the cDNA of ATCC Deposit No. 75803.

7. The polynucleotide of Claim 1 having the coding sequence of Ckβ-9 as shown in Figure 1.

8. The polynucleotide of Claim 2 having the coding sequence of Ckβ-9 deposited as ATCC Deposit No. 75803

9. A vector containing the DNA of Claim 2.

10. A host cell genetically engineered with the vector of Claim 9.

11. A process for producing a polypeptide comprising: expressing from the host cell of Claim 10 the polypeptide encoded by said DNA.

12. A process for producing cells capable of expressing a polypeptide comprising genetically engineering cells with the vector of Claim 9.

13. An isolated DNA hybridizable to the DNA of Claim 2 and encoding a polypeptide having Ckβ-9 activity.

14. A polypeptide selected from the group consisting of (i) a Ckβ-9 polypeptide having the deduced amino acid sequence of Figure 1 and fragments, analogs and derivatives thereof; and (ii) a Ckβ-9 polypeptide encoded by the cDNA of ATCC Deposit No. 75803 and fragments, analogs and derivatives of said polypeptide

15. The polypeptide of Claim 14 wherein the polypeptide is Ckβ-9 having the deduced amino acid sequence of Figure 1.

16. Antibodies against the polypeptides of claim 14.

17. Antagonists against the polypeptides of claim 14.

18. A method for the treatment of a patient having need of Ckβ-9 comprising: administering to the patient a therapeutically effective amount of the polypeptide of claim 14.

19. A method for the treatment of a patient having need to inhibit Ckβ-9 comprising: administering to the patient a therapeutically effective amount of the antagonist of Claim 14.

20. A pharmaceutical composition comprising any one of the polypeptides of Claim 14 and a pharmaceutically acceptable carrier.

21. The method of Claim 18 wherein said therapeutically effective amount of the polypeptide is administered by providing to the patient DNA encoding said polypeptide and expressing said polypeptide *in vivo*.

ABSTRACT OF THE DISCLOSURE

Human chemokine polypeptides and DNA (RNA) encoding such chemokine polypeptides and a procedure for producing such polypeptides by recombinant techniques is disclosed. Also disclosed are methods for utilizing such chemokine polypeptides for the treatment of leukemia, tumors, chronic infections, autoimmune disease, fibrotic disorders, wound healing and psoriasis. Antagonists against such chemokine polypeptides and their use as a therapeutic to treat rheumatoid arthritis, autoimmune and chronic inflammatory and infective diseases, allergic reactions, prostaglandin-independent fever and bone marrow failure are also disclosed.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: LI, ET AL.

(ii) TITLE OF INVENTION: Human Chemokine Beta-9

(iii) NUMBER OF SEQUENCES: 6

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI, STEWART & OLSTEIN

(B) STREET: 6 BECKER FARM ROAD

(C) CITY: ROSELAND

(D) STATE: NEW JERSEY

(E) COUNTRY: USA

(F) ZIP: 07068

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 3.5 INCH DISKETTE

(B) COMPUTER: IBM PS/2

(C) OPERATING SYSTEM: MS-DOS

(D) SOFTWARE: WORD PERFECT 5.1

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE: Concurrently

(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA

(A) APPLICATION NUMBER:

(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: PERRARO, GREGORY D.
(B) REGISTRATION NUMBER: 36,134
(C) REFERENCE/DOCKET NUMBER: 325800-183

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 201-994-1700
(B) TELEFAX: 201-994-1744

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 405 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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ATGGCTCAGT CACTGGCTCT GAGCCTCCTT ATCCTGGTTC TGGCCTTTGG CATCCCCAGG    60
ACCCAAGGCA GTGATGGAGG GGCTCAGGAC TGTTGCCTCA AGTACAGCCA AAGGAAGATT   120
CCCGCCAAGG TTGTCCGCAG CTACCGGAAG CAGGAACCAA GCTTAGGCTG CTCCATCCCA   180
GCTATCCTGT TCTTGCCCCG CAAGCGCTCT CAGGCAGAGC TATGTGCAGA CCCAAAGGAG   240
CTCTGGGTGC ACCAGCTGAT GCAGCATCTG GACAAGACAC CATCCCCACA GAAACCAGCC   300
CAGGGCTGCA GGAAGGACAG GCGGGCCTCC AAGACTGGCA AGAAAGGAAA GGGCTCCAAA   360
GGCTGCAAGA GGACTGACCG GTCACAGACC CCTAAAGGGC CATAG                   405
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(3) INFORMATION FOR SEQ ID NO:2:
(i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 134 AMINO ACIDS
(B) TYPE: AMINO ACID
(C) STRANDEDNESS:
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

nt. 244-246 = TGG = W
nt. 284 = C (no "T" insert)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Gln Ser Leu Ala Leu Ser Leu Leu Ile Leu Val Leu Ala
-20 -15 -10
Phe Gly Ile Pro Arg Thr Gln Gly Ser Asp Gly Gly Ala Gln Asp
-5 1 5
Cys Cys Leu Lys Tyr Ser Gln Arg Lys Ile Pro Ala Lys Val Val
10 15 20
Arg Ser Tyr Arg Lys Gln Glu Pro Ser Leu Gly Cys Ser Ile Pro
25 30 35
Ala Ile Leu Phe Leu Pro Arg Lys Arg Ser Gln Ala Glu Leu Cys
40 45 50
Ala Asp Pro Lys Glu Leu Tyr Val Gln Gln Leu Met Gln His Leu
55 60 65
Asp Lys Thr Pro Ser Pro Gln Lys Pro Ala Gln Gly Cys Arg Lys
70 75 80
Asp Arg Gly Ala Ser Lys Thr Gly Lys Lys Gly Lys Gly Ser Lys
85 90 95
Gly Cys Lys Arg Thr Glu Arg Ser Gln Thr Pro Lys Gly Pro
100 105 110

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 26 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCCGCATGCG TGATGGAGGG GCTCAG 26

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 30 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

AAAGGATCCT GGCCCTTTAG GGGTCTGTGA 30

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 27 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AAAGGATCCA GACATGGCTC AGTCACT 27

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 57 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CGCTCTAGAT CAAGCGTAGT CTGGGACGTC GTATGGGTAT GGCCCTTTAG GGGTCTG 57

ATGGCTCAGTCACTGGCTCTGAGCCTCCTTATCCTGGTTCTGGCCTTTGGCATCCCCAGG
M A Q S L A L S L L I L V L A F G I P R

ACCCAAGCCAGTCATGCAGGGGCTCAGGACTGTTGCCTCAAGTACAGCCAAAGCAAGATT
T Q G S D G G A Q D C C L K Y S Q R K I

CCCGCCAACGTTGTCCGCAGCTACCGGAAGCAGCAACCAAGCTTAGGCTGCTCCATCCCA
P A K V V R S Y R K Q E P S L G C S I P

GCTATCCTGTTCTTGCCCCCGCAAGCGCTCTCAGGCAGAGCTATGTGCAGACCCAAAGGAG
A I L F L P R K R S Q A E L C A D P K E

CTCTGGGTGCAGCAGCTGATGCAGCATCTGGACAAGACACCATCCCCACAGAAACCAGCC
L W V Q Q L M Q H L D K T P S P Q K P A

CAGGCCTGCAGGAAGGACAGGGGGGCCTCCAAGACTGGCAAGAAACGAAAGGGCTCCAAA
Q G C R K D R G A S K T G K K G K G S K

CGCTGCAAGAGCACTCAGCGGTCACAGACCCCTAAAGGGCCATAG
C C K R T E R S Q T P K G P *

FIGURE 1

25 DGCAQDCCLKYSQ.P..IPAKV/RSYRKQEPSLGCSIPAILFLPRKRSQAE 73
.| : .||:: . || .:.|| | .| |. .||:| .:.:
2 PG:PRACCFRVTNICKISPQALKSY.KIITSSKCPQTAIVF..E:KPDKH 49

74 LCADPKELWVCQLMQnLD.TPSPQ?? 99
.|||:: .||: .:
49 ICADPRXXWVQDAKKYLDQISQX:KP 74

FIG. 4

DECLARATION FOR PATENT APPLICATION

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name

I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled:

HUMAN CHEMOKINE BETA-9

the specification of which ( ) is attached hereto or (X) was filed on August 23, 1994 as Application Serial No. 08/294,254 and was amended on _____ (if applicable).

I hereby state that I have reviewed and understand the contents of the above identified specification, including the claims, as amended by any amendment referred to above.

I acknowledge the duty to disclose information which is material to the examination of this application in accordance with Title 37, Code of Federal Regulations, Section 1.56(a).

I hereby claim foreign priority benefits under Title 35, United States Code, Section 119 of any foreign application(s) for patent or inventor's certificate listed below and have also identified below any foreign application for patent or inventor's certificate having a filing date before that of the application on which priority is claimed: Prior Foreign Application(s).

			Priority Claimed	
None (Number)	(Country)	(Day/Month/Year Filed)	Yes	No
(Number)	(Country)	(Day/Month/Year Filed)	Yes	No

I hereby claim the benefit under Title 35, United States Code, Section 120 of any United States application(s) listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States application in the manner provided by the first paragraph of Title 35, United States Code, Section 112, I acknowledge the duty to disclose material information as defined in Title 37, Code of Federal Regulations, Section 1.56(a) which occurred between the filing date of the prior application and the national or PCT international filing date of this application:

None (Application Serial No.)	(Filing Date)	(Status: patented, pending, abandoned)
(Application Serial No.)	(Filing Date)	(Status: patented, pending, abandoned)

I hereby appoint the following attorney(s) and/or agent(s) to prosecute this application and to transact all business in the Patent and Trademark Office connected therewith: John N. Bain (Reg. No. 18,651); John C. Gilfillan, III (Reg. No. 22,736); Elliot M. Olstein (Reg. No. 24,025); Raymond J. Lillie (Reg. No. 31,778); Charles J. Herron (Reg. No. 28,019); Gregory Ferraro (Reg. No. 36,134) and William Squire (Reg. No. 25,378). Address correspondence and telephone calls to: Charles J. Herron c/o Carella, Byrne, Bain, Gilfillan, Cecchi, Stewart & Olstein, 6 Becker Farm Road, Roseland, NJ 07068 - (201) 994-1700.

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

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Inventor's signature: _____ Date: 12/14/01
Residence: 11011B Tiedge Drive Gaithersburg MD 20878 Citizenship: PRC
Post Office Address: _____

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Inventor's signature: _____ Date: 12/14/01
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Post Office Address: _____

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Docket No. 21400.01

HGS_SEQ_ID_NO:2_'251_appl.1st
HGS_SEQ_ID_NO:2_'251_appl.2nd

CLUSTAL W (1.82) Multiple Sequence Alignments

```
Sequence format is Pearson
Sequence 1: HGS_SEQ_ID_NO_2_'251_appl.1st      125 aa
Sequence 2: HGS_SEQ_ID_NO_2_'251_appl.2nd      134 aa
Start of Pairwise alignments
Aligning...
Sequences (1:2) Aligned. Score:  79
Guide tree        file created:   [baayUaqSb.dnd]
Start of Multiple Alignment
There are 1 groups
Aligning...
Group 1: Sequences:   2      Score:2426
Alignment Score 598
CLUSTAL-Alignment file created  [baayUaqSb.aln]
CLUSTAL W (1.82) multiple sequence alignment


HGS_SEQ_ID_NO_2_'251_appl.1st      MAQSLALSLLILVLAFGIPRTQGSDGGAQDCCLKYSQRKIPAKVVRSYRK
HGS_SEQ_ID_NO_2_'251_appl.2nd      MAQSLALSLLILVLAFGIPRTQGSDGGAQDCCLKYSQRKIPAKVVRSYRK
                                   **************************************************

HGS_SEQ_ID_NO_2_'251_appl.1st      QEPSLGCSIPAILFLPRKRSQAELCADPKELYVQQLMQHLDKTPFPTETS
HGS_SEQ_ID_NO_2_'251_appl.2nd      QEPSLGCSIPAILFLPRKRSQAELCADPKELYVQQLMQHLDKTPSPQKPA
                                   ******************************************** * :.:

HGS_SEQ_ID_NO_2_'251_appl.1st      PGLQEGQGGLQDWQERKG------LQRLQED---
HGS_SEQ_ID_NO_2_'251_appl.2nd      QGCRKDRGASKTGKKGKGSKGCKRTERSQTPKGP
                                    * ::.:*. :  :: **       :* *
```

HGS_SEQ_ID_NO:1_'251_appl.1st
HGS_SEQ_ID_NO:1_'251_appl.2nd

CLUSTAL W (1.82) Multiple Sequence Alignments

Sequence format is Pearson
Sequence 1: HGS_SEQ_ID_NO_1_'251_appl.1st 378 bp
Sequence 2: HGS_SEQ_ID_NO_1_'251_appl.2nd 405 bp
Start of Pairwise alignments
Aligning...
Sequences (1:2) Aligned. Score: 99
Guide tree file created: [baayBay3b.dnd]
Start of Multiple Alignment
There are 1 groups
Aligning...
Group 1: Sequences: 2 Score:7126
Alignment Score 2850
CLUSTAL-Alignment file created [baayBay3b.aln]
CLUSTAL W (1.82) multiple sequence alignment

```
HGS_SEQ_ID_NO_1_'251_appl.1st      ATGGCTCAGTCACTGGCTCTGAGCCTCCTTATCCTGGTTCTGGCCTTTGG
HGS_SEQ_ID_NO_1_'251_appl.2nd      ATGGCTCAGTCACTGGCTCTGAGCCTCCTTATCCTGGTTCTGGCCTTTGG
                                   *************************************************

HGS_SEQ_ID_NO_1_'251_appl.1st      CATCCCCAGGACCCAAGGCAGTGATGGAGGGGCTCAGGACTGTTGCCTCA
HGS_SEQ_ID_NO_1_'251_appl.2nd      CATCCCCAGGACCCAAGGCAGTGATGGAGGGGCTCAGGACTGTTGCCTCA
                                   *************************************************

HGS_SEQ_ID_NO_1_'251_appl.1st      AGTACAGCCAAAGGAAGATTCCCGCCAAGGTTGTCCGCAGCTACCGGAAG
HGS_SEQ_ID_NO_1_'251_appl.2nd      AGTACAGCCAAAGGAAGATTCCCGCCAAGGTTGTCCGCAGCTACCGGAAG
                                   *************************************************

HGS_SEQ_ID_NO_1_'251_appl.1st      CAGGAACCAAGCTTAGGCTGCTCCATCCCAGCTATCCTGTTCTTGCCCCG
HGS_SEQ_ID_NO_1_'251_appl.2nd      CAGGAACCAAGCTTAGGCTGCTCCATCCCAGCTATCCTGTTCTTGCCCCG
                                   *************************************************

HGS_SEQ_ID_NO_1_'251_appl.1st      CAAGCGCTCTCAGGCAGAGCTATGTGCAGACCCAAAGGAGCTCTGGGTGC
HGS_SEQ_ID_NO_1_'251_appl.2nd      CAAGCGCTCTCAGGCAGAGCTATGTGCAGACCCAAAGGAGCTCTGGGTGC
                                   *************************************************

HGS_SEQ_ID_NO_1_'251_appl.1st      AGCAGCTGATGCAGCATCTGGACAAGACACCATTCCCCACAGAAACCAGC
HGS_SEQ_ID_NO_1_'251_appl.2nd      AGCAGCTGATGCAGCATCTGGACAAGACACCAT-CCCCACAGAAACCAGC
                                   ********************************** ***************

HGS_SEQ_ID_NO_1_'251_appl.1st      CCAGGGCTGCAGGAAGGACAGGGGGGCCTCCAAGACTGGCAAGAAAGGAA
HGS_SEQ_ID_NO_1_'251_appl.2nd      CCAGGGCTGCAGGAAGGACAGGGGGGCCTCCAAGACTGGCAAGAAAGGAA
                                   *************************************************

HGS_SEQ_ID_NO_1_'251_appl.1st      AGGGCTCCAAAGGCTGCAAGAGGACTGA----------------------
HGS_SEQ_ID_NO_1_'251_appl.2nd      AGGGCTCCAAAGGCTGCAAGAGGACTGAGCGGTCACAGACCCCTAAAGGG
                                   ***************************

HGS_SEQ_ID_NO_1_'251_appl.1st      ------
HGS_SEQ_ID_NO_1_'251_appl.2nd      CCATAG
```

INCY_SEQ_ID_NO:3_'740_appl.
HGS_SEQ_ID_NO:1_'251_appl.

CLUSTAL W (1.82) Multiple Sequence Alignments

```
Sequence format is Pearson
Sequence 1: INCY_SEQ_ID_NO_3_'740_appl.       402 bp
Sequence 2: HGS_SEQ_ID_NO_1_'251_appl.        378 bp
Start of Pairwise alignments
Aligning...
Sequences (1:2) Aligned. Score:  99
Guide tree        file created:   [baaetaigY.dnd]
Start of Multiple Alignment
There are 1 groups
Aligning...
Group 1: Sequences:   2      Score:7126
Alignment Score 2850
CLUSTAL-Alignment file created  [baaetaigY.aln]
CLUSTAL W (1.82) multiple sequence alignment


INCY_SEQ_ID_NO_3_'740_appl.       ATGGCTCAGTCACTGGCTCTGAGCCTCCTTATCCTGGTTCTGGCCTTTGG
HGS_SEQ_ID_NO_1_'251_appl.        ATGGCTCAGTCACTGGCTCTGAGCCTCCTTATCCTGGTTCTGGCCTTTGG
                                  **************************************************

INCY_SEQ_ID_NO_3_'740_appl.       CATCCCCAGGACCCAAGGCAGTGATGGAGGGGCTCAGGACTGTTGCCTCA
HGS_SEQ_ID_NO_1_'251_appl.        CATCCCCAGGACCCAAGGCAGTGATGGAGGGGCTCAGGACTGTTGCCTCA
                                  **************************************************

INCY_SEQ_ID_NO_3_'740_appl.       AGTACAGCCAAAGGAAGATTCCCGCCAAGGTTGTCCGCAGCTACCGGAAG
HGS_SEQ_ID_NO_1_'251_appl.        AGTACAGCCAAAGGAAGATTCCCGCCAAGGTTGTCCGCAGCTACCGGAAG
                                  **************************************************

INCY_SEQ_ID_NO_3_'740_appl.       CAGGAACCAAGCTTAGGCTGCTCCATCCCAGCTATCCTGTTCTTGCCCCG
HGS_SEQ_ID_NO_1_'251_appl.        CAGGAACCAAGCTTAGGCTGCTCCATCCCAGCTATCCTGTTCTTGCCCCG
                                  **************************************************

INCY_SEQ_ID_NO_3_'740_appl.       CAAGCGCTCTCAGGCAGAGCTATGTGCAGACCCAAAGGAGCTCTGGGTGC
HGS_SEQ_ID_NO_1_'251_appl.        CAAGCGCTCTCAGGCAGAGCTATGTGCAGACCCAAAGGAGCTCTGGGTGC
                                  **************************************************

INCY_SEQ_ID_NO_3_'740_appl.       AGCAGCTGATGCAGCATCTGGACAAGACACCAT-CCCCACAGAAACCAGC
HGS_SEQ_ID_NO_1_'251_appl.        AGCAGCTGATGCAGCATCTGGACAAGACACCATTCCCCACAGAAACCAGC
                                  ********************************** ***************

INCY_SEQ_ID_NO_3_'740_appl.       CCAGGGCTGCAGGAAGGACAGGGGGGCCTCCAAGACTGGCAAGAAAGGAA
HGS_SEQ_ID_NO_1_'251_appl.        CCAGGGCTGCAGGAAGGACAGGGGGGCCTCCAAGACTGGCAAGAAAGGAA
                                  **************************************************

INCY_SEQ_ID_NO_3_'740_appl.       AGGGCTCCAAAGGCTGCAAGAGGACTGAGCGGTCACAGACCCCTAAAGGG
HGS_SEQ_ID_NO_1_'251_appl.        AGGGCTCCAAAGGCTGCAAGAGGACTGA----------------------
                                  ***************************

INCY_SEQ_ID_NO_3_'740_appl.       CCA
HGS_SEQ_ID_NO_1_'251_appl.        ---
```

INCY_SEQ_ID_NO:4_'740_appl.
HGS_SEQ_ID_NO:2_'251_appl.

CLUSTAL W (1.82) Multiple Sequence Alignments

```
Sequence format is Pearson
Sequence 1: INCY_SEQ_ID_NO_4_'740_appl.      134 aa
Sequence 2: HGS_SEQ_ID_NO_2_'251_appl.       134 aa
Start of Pairwise alignments
Aligning...
Sequences (1:2) Aligned. Score:  99
Guide tree        file created:   [baakLaW4a.dnd]
Start of Multiple Alignment
There are 1 groups
Aligning...
Group 1: Sequences:   2      Score:2903
Alignment Score 822
CLUSTAL-Alignment file created  [baakLaW4a.aln]
CLUSTAL W (1.82) multiple sequence alignment


INCY_SEQ_ID_NO_4_'740_appl.      MAQSLALSLLILVLAFGIPRTQGSDGGAQDCCLKYSQRKIPAKVVRSYRK
HGS_SEQ_ID_NO_2_'251_appl.       MAQSLALSLLILVLAFGIPRTQGSDGGAQDCCLKYSQRKIPAKVVRSYRK
                                 **************************************************

INCY_SEQ_ID_NO_4_'740_appl.      QEPSLGCSIPAILFLPRKRSQAELCADPKELWVQQLMQHLDKTPSPQKPA
HGS_SEQ_ID_NO_2_'251_appl.       QEPSLGCSIPAILFLPRKRSQAELCADPKELYVQQLMQHLDKTPSPQKPA
                                 ********************************:*****************

INCY_SEQ_ID_NO_4_'740_appl.      QGCRKDRGASKTGKKGKGSKGCKRTERSQTPKGP
HGS_SEQ_ID_NO_2_'251_appl.       QGCRKDRGASKTGKKGKGSKGCKRTERSQTPKGP
                                 **********************************
```